



#14

# SEQUENCE LISTING

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<120> MAMMALIAN CYTOKINES; RECEPTORS; RELATED REAGENTS AND METHODS

<130> dx01341

<140> 10/008566

<141> 2001-11-08

<150> US 60/298268

<151> 2001-06-14

<150> US 60/247218

<151> 2000-11-10

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<170> PatentIn version 3.1

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Asn Gly Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys  
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Tyr Ser Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys Ala  
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ttt gag gac cca gat gtc aac acc acc aat ctg gaa ttt gaa ata tgt 244  
Phe Glu Asp Pro Asp Val Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys  
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ggg gcc ctc gtg gag gta aag tgc ctg aat ttc agg aaa cta caa gag 292  
Gly Ala Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu  
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Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn	
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ata tgt gtg aag gtt gga gaa aag agt cta acc tgc aaa aaa ata gac	388
Ile Cys Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp	
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cta acc act ata gtt aaa cct gag gct cct ttt gac ctg agt gtc atc	436
Leu Thr Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Ile	
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tat cgg gaa gga gcc aat gac ttt gtg gtg aca ttt aat aca tca cac	484
Tyr Arg Glu Gly Ala Asn Asp Phe Val Val Thr Phe Asn Thr Ser His	
140 145 150	
ttg caa aag aag tat gta aaa gtt tta atg cat gat gta gct tac cgc	532
Leu Gln Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr Arg	
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cag gaa aag gat gaa aac aaa tgg acg cat gtg aat tta tcc agc aca	580
Gln Glu Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr	
175 180 185	
aag ctg aca ctc ctg cag aga aag ctc caa ccg gca gca atg tat gag	628
Lys Leu Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu	
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Ile Lys Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser	
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gaa tgg agt cca agt tat tac ttc aga act cca gag atc aat aat agc	724
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tca ggg gag atg gat cct atc tta cta acc atc agc att ttg agt ttt	772
Ser Gly Glu Met Asp Pro Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe	
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Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys	
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agg att aag cct atc gta tgg ccc agt ctc ccc gat cat aag aag act	868
Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr	
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ctg gaa cat ctt tgt aag aaa cca aga aaa aat tta aat gtg agt ttc	916
Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe	
285 290 295	
aat cct gaa agt ttc ctg gac tgc cag att cat agg gtg gat gac att	964
Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile	
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caa gct aga gat gaa gtg gaa ggt ttt ctg caa gat acg ttt cct cag	1012
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ccc aac tgc cca tct gag gat gta gtc gtc act cca gaa agc ttt gga	1108
Pro Asn Cys Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly	
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aga gat tca tcc ctc aca tgc ctg gct ggg aat gtc agt gca tgt gac	1156
Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp	
365 370 375	
gcc cct att ctc tcc tct tcc agg tcc cta gac tgc agg gag agt ggc	1204
Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly	
380 385 390	
aag aat ggg cct cat gtg tac cag gac ctc ctg ctt agc ctt ggg act	1252
Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr	
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aca aac agc acg ctg ccc cct cca ttt tct ctc caa tct gga atc ctg	1300
Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu	
415 420 425	
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Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly	
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Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn	
445 450 455	
cag tgaagtgtaa gaaaccaga ctgaacttac cgtgagcgac aaagatgatt	1449
Gln	
taaaagggaa gtctagagtt cctagtctcc ctcacagcac agagaagaca aaattagcaa	1509
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35		40		45
Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val	50	55	60	
Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val	65	70	75	80
Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr	85	90	95	
Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly	100	105	110	
Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys	115	120	125	
Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn	130	135	140	
Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val	145	150	155	160
Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn	165	170	175	
Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln	180	185	190	
Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile	195	200	205	
Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr	210	215	220	
Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro	225	230	235	240
Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu	245	250	255	
Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val	260	265	270	
Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys	275	280	285	

Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu  
 290 295 300

Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val  
 305 310 315 320

Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu  
 325 330 335

Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu  
 340 345 350

Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr  
 355 360 365

Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser  
 370 375 380

Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val  
 385 390 395 400

Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro  
 405 410 415

Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala  
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Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala  
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gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp 80 85 90	291
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tcc tac ggg gat ctc ctc tat gag gtt cag tac cgg agc ccc ttc gac Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp 145 150 155	483
acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu 160 165 170	531
ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala 175 180 185	579
atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu 190 195 200 205	627
gtg aca tgc tgg cag aga ggc gag att cgg gat gcc tgt gca gag aca Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr 210 215 220	675
cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser 225 230 235	723
ctg gcc atc ctt ctg atg gtg tct ctc ctc ctt ctg tct tta tgg aaa Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys 240 245 250	771

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Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys	
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tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag	867
Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu	
270 275 280 285	
tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt	915
Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly	
290 295 300	
gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc	963
Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala	
305 310 315	
aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag	1011
Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu	
320 325 330	
aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa	1059
Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln	
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ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac	1107
Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp	
350 355 360 365	
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Arg Ser Tyr Val Ala Leu	
370	
caggatccac gttgacattt aaagacagag gggactgtcc cggggactcc acaccacat	1215
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cttgatggca gatgggagcc aattgctcca ggagatttac tcccagttcc ttttcgtgcc	1395
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35 40 45

Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
50 55 60

Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
65 70 75 80

Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr  
85 90 95

Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
100 105 110

Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
115 120 125

Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
130 135 140

Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
145 150 155 160

Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
165 170 175

Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
180 185 190

Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
195 200 205

Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
210 215 220

Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
225 230 235 240

Leu Leu Met Val Ser Leu Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
245 250 255

Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
260 265 270



Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 275 280 285

Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
 290 295 300

Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
 305 310 315 320

Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 325 330 335

Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
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Val Ala Leu  
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 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr  
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 Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser  
 35 40 45  
 aaa gac ctg att aca tat atg agt ggg acc aaa agt acc gag ttc aac 192  
 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn  
 50 55 60  
 aac acc gtc tct tgt agc aat cgg cca cat tgc ctt act gaa atc cag 240  
 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln  
 65 70 75 80  
 agc cta acc ttc aat ccc acc gcc ggc tgc gcg tcg ctc gcc aaa gaa 288

Ser	Leu	Thr	Phe	Asn	Pro	Thr	Ala	Gly	Cys	Ala	Ser	Leu	Ala	Lys	Glu	
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atg	ttc	gcc	atg	aaa	act	aag	gct	gcc	tta	gct	atc	tgg	tgc	cca	ggc	336
Met	Phe	Ala	Met	Lys	Thr	Lys	Ala	Ala	Leu	Ala	Ile	Trp	Cys	Pro	Gly	
			100					105					110			
tat	tcg	gaa	act	cag	ata	aat	gct	act	cag	gca	atg	aag	aag	agg	aga	384
Tyr	Ser	Glu	Thr	Gln	Ile	Asn	Ala	Thr	Gln	Ala	Met	Lys	Lys	Arg	Arg	
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aaa	agg	aaa	gtc	aca	acc	aat	aaa	tgt	ctg	gaa	caa	gtg	tca	caa	tta	432
Lys	Arg	Lys	Val	Thr	Thr	Asn	Lys	Cys	Leu	Glu	Gln	Val	Ser	Gln	Leu	
		130				135					140					
caa	gga	ttg	tgg	cgt	cgc	ttc	aat	cga	cct	tta	ctg	aaa	caa	cag	taa	480
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Asn	Cys	Asp	Phe	Glu	Lys	Ile	Lys	Ala	Ala	Tyr	Leu	Ser	Thr	Ile	Ser	
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Lys	Asp	Leu	Ile	Thr	Tyr	Met	Ser	Gly	Thr	Lys	Ser	Thr	Glu	Phe	Asn	
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Asn	Thr	Val	Ser	Cys	Ser	Asn	Arg	Pro	His	Cys	Leu	Thr	Glu	Ile	Gln	
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Ser	Leu	Thr	Phe	Asn	Pro	Thr	Ala	Gly	Cys	Ala	Ser	Leu	Ala	Lys	Glu	
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Tyr	Ser	Glu	Thr	Gln	Ile	Asn	Ala	Thr	Gln	Ala	Met	Lys	Lys	Arg	Arg	
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Lys	Arg	Lys	Val	Thr	Thr	Asn	Lys	Cys	Leu	Glu	Gln	Val	Ser	Gln	Leu	
	130					135					140					

Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu Lys Gln Gln  
145 150 155